# **Resource Summary Report**

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# **GASSST**

RRID:SCR\_004413 Type: Tool

**Proper Citation** 

GASSST (RRID:SCR\_004413)

#### **Resource Information**

URL: http://www.irisa.fr/symbiose/projects/gassst/

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**Description:** Software that finds global alignments of short DNA sequences against large DNA banks. It is able to perform fast gapped alignments and works well for both short and longer reads. It has been tested for reads up to 500bp.

Abbreviations: GASSST

**Synonyms:** GASSST : Global Alignment Short Sequence Search Tool, Global Alignment Short Sequence Search Tool

Resource Type: software resource

Defining Citation: PMID:20739310

Keywords: bio.tools

**Funding:** 

Availability: CeCILL license, v2

Resource Name: GASSST

Resource ID: SCR\_004413

Alternate IDs: biotools:gassst, OMICS\_00663

Alternate URLs: https://bio.tools/gassst

Record Creation Time: 20220129T080224+0000

Record Last Update: 20250420T014220+0000

## **Ratings and Alerts**

No rating or validation information has been found for GASSST.

No alerts have been found for GASSST.

## Data and Source Information

Source: SciCrunch Registry

#### **Usage and Citation Metrics**

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Alser M, et al. (2021) Technology dictates algorithms: recent developments in read alignment. Genome biology, 22(1), 249.

Bush SJ, et al. (2021) Generalizable characteristics of false-positive bacterial variant calls. Microbial genomics, 7(8).

Xuan B, et al. (2021) Draft genome of the Korean smelt Hypomesus nipponensis and its transcriptomic responses to heat stress in the liver and muscle. G3 (Bethesda, Md.), 11(9).

You I, et al. (2020) Genome-based species-specific primers for rapid identification of six species of Lactobacillus acidophilus group using multiplex PCR. PloS one, 15(3), e0230550.

Li G, et al. (2020) Genome-wide identification and analysis of highly specific CRISPR/Cas9 editing sites in pepper (Capsicum annuum L.). PloS one, 15(12), e0244515.

Xu J, et al. (2017) Altered expression profiles of microRNA families during de-etiolation of maize and rice leaves. BMC research notes, 10(1), 108.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.